



SEQUENCE LISTING

#11

<110> Prayaga, Sudhirdas
Shimkets, Richard

<120> NOVEL INTERFERON OMEGA AND NUCLEIC ACIDS ENCODING SAME

<130> 15966-615

<140> 09/732,436

<141> 2000-12-07

<150> 60/169,887

<151> 1999-12-09

<150> 60/170,230

<151> 1999-12-10

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Curagen clone
AC015663_A

<400> 1

Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
1 5 10 15

Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
20 25 30

Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
35 40 45

Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys
50 55 60

Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys
65 70 75 80

Ala Gly Gly Thr Gly Ala Thr Thr Thr Cys Thr Gly Cys Cys Cys Thr

	85		90		95
Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly	100		105		110
Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr	115		120		125
Thr Thr Thr Thr Ala Cys Ala Cys Ala Ala Gly Gly Gly Cys Thr Thr	130		135		140
Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr	145		150		155
					160
Ala Gly Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala	165		170		175
Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr	180		185		190
Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala	195		200		205
Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr	210		215		220
Thr Thr Gly Gly Thr Ala Thr Ala Gly Ala Gly Gly Ala Thr Gly Gly	225		230		235
					240
Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys	245		250		255
Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Gly Cys Cys	260		265		270
Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala	275		280		285
Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Gly Ala	290		295		300
Gly Thr Ala Cys Ala Thr Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala	305		310		315
					320
Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala Ala Thr Thr Cys Ala Gly	325		330		335
Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Gly Ala Gly					

340 345 350
 Gly Thr Thr Gly Thr Cys Gly Thr Ala Ala Thr Gly Gly Thr Ala Ala
 355 360 365
 Ala Gly Gly Gly Ala Thr Thr Thr Thr Thr Cys Thr Thr Ala Ala Gly
 370 375 380
 Cys Ala Cys Ala Ala Ala Ala Cys Thr Thr Cys Ala Ala Gly Ala Ala
 385 390 395 400
 Ala Ala Ala Gly Ala Gly Ala Ala Cys Ala Gly Ala Ala Gly Ala Ala
 405 410 415
 Ala Ala Gly Ala Gly Ala Ala Cys Thr Gly Cys Ala Ala Ala Ala Ala
 420 425 430
 Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly Thr Ala
 435 440 445
 Ala Thr Cys Thr Ala Thr Thr Thr Ala Gly Cys Ala Gly Ala Ala Gly
 450 455 460
 Ala Gly Thr Gly Ala Ala Ala Gly Cys Thr Gly
 465 470 475

<210> 2
 <211> 610
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Curagen clone

<400> 2
 Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
 1 5 10 15
 Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
 20 25 30
 Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
 35 40 45
 Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys
 50 55 60

Gly	Ala	Cys	Cys	Thr	Gly	Cys	Cys	Thr	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	65	70	75	80
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	85	90	95	
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	100	105	110	
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	115	120	125	
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	130	135	140	
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	145	150	155	160
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	165	170	175	
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	180	185	190	
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	195	200	205	
Ala	Ala	Ala	Gly	Cys	Thr	Cys	Ala	Gly	Gly	Thr	Gly	Ala	Thr	Thr	Thr	Thr	210	215	220	
Cys	Thr	Gly	Cys	Cys	Cys	Thr	Cys	Cys	Ala	Thr	Ala	Ala	Gly	Ala	Thr	Thr	225	230	235	240
Gly	Cys	Ala	Cys	Cys	Ala	Gly	Cys	Ala	Gly	Ala	Thr	Cys	Thr	Thr	Cys	Cys	245	250	255	
Ala	Gly	Cys	Cys	Thr	Cys	Thr	Thr	Thr	Thr	Thr	Ala	Cys	Ala	Cys	Ala	Ala	260	265	270	
Ala	Gly	Gly	Gly	Cys	Thr	Thr	Gly	Thr	Cys	Thr	Gly	Ala	Thr	Gly	Cys	Cys	275	280	285	
Thr	Thr	Gly	Gly	Ala	Ala	Thr	Ala	Gly	Gly	Gly	Cys	Cys	Thr	Thr	Cys	Cys	290	295	300	
Cys	Thr	Gly	Gly	Ala	Cys	Ala	Ala	Ala	Cys	Thr	Cys	Cys	Ala	Gly	Ala	Ala	305	310	315	320

Cys Thr Gly Gly Ala Thr Thr Thr Cys Ala Thr Cys Ala Gly Cys Ala
 325 330 335
 Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys Thr Gly Gly Ala Gly
 340 345 350
 Ala Cys Cys Thr Gly Cys Thr Thr Thr Gly Gly Thr Ala Thr Ala Gly
 355 360 365
 Ala Gly Gly Ala Thr Gly Gly Gly Ala Ala Gly Cys Ala Ala Gly Ala
 370 375 380
 Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly Ala Ala Ala Thr Thr
 385 390 395 400
 Gly Ala Gly Gly Gly Cys Cys Cys Thr Ala Cys Ala Cys Thr Gly Gly
 405 410 415
 Cys Cys Ala Thr Ala Ala Ala Gly Ala Gly Gly Thr Ala Cys Thr Thr
 420 425 430
 Cys Cys Ala Gly Gly Gly Ala Gly Thr Ala Cys Ala Thr Thr Thr Cys
 435 440 445
 Thr Thr Cys Thr Thr Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Ala
 450 455 460
 Ala Ala Thr Thr Cys Ala Gly Gly Ala Ala Cys Thr Gly Thr Ala Cys
 465 470 475 480
 Cys Thr Gly Gly Gly Ala Gly Gly Thr Thr Gly Thr Cys Gly Thr Ala
 485 490 495
 Ala Thr Gly Gly Thr Ala Ala Ala Gly Gly Gly Ala Thr Thr Thr Thr
 500 505 510
 Thr Cys Thr Thr Ala Ala Gly Cys Ala Cys Ala Ala Ala Ala Cys Thr
 515 520 525
 Thr Cys Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys
 530 535 540
 Ala Gly Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys Thr
 545 550 555 560
 Gly Cys Ala Ala Ala Ala Ala Ala Ala Ala Thr Cys Thr Gly Gly Ala
 565 570 575

Ala Ala Ala Gly Gly Thr Ala Ala Thr Cys Thr Ala Thr Thr Thr Ala
580 585 590

Gly Cys Ala Gly Ala Ala Gly Ala Gly Thr Gly Ala Ala Ala Gly Cys
595 600 605

Thr Gly
610

<210> 3
<211> 1887
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Curagen clone
AF038458_A

<400> 3
atggccatcc tcccgttgct cctgtgcttg ctgccgctgg cccctgcctc atccccaccc 60
cagtcagcca caccagccc atgtcccgc cgtgcgcgt gccagacaca gtcgctgccc 120
ctaagcgtgc tgtgccagg ggcaggcctc ctgttcgtgc caccctcgtt ggaccgccc 180
gcagccgagc tgcggctggc agacaacttc atgcctccg tgcgcccgcg cgacctggcc 240
aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
ggcgcccttc cgcacctgcg ggccctgcgt gccctgcacc tggatggcaa ccggctgacc 360
tcaactggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420
aaccagctgg cagcgtggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggcctggg ccgcctgggc 540
aacgtcaaca cgttgggcct cgaccacaac ctgctggctt ctgtgccgcg cggcgctttt 600
tccgcctgc acaagctggc ccggctggac atgacctcca accgcctgac cacaatccca 660
cccgacccac tcttctcccg cctgcccctg ctgcgccagg cccggggctc gccgcctct 720
gccctggtgc tggccttttg cgggaacccc ctgcaactga actgcgagct ggtgtggctg 780
cgtgccttg cgcgaggga cgacctcgag gcctgcgcgt cccacctgc tctgggcggc 840
cgctacttct gggcggtggg cgaggaggag tttgtctgcg agccgcccgt ggtgactcac 900
cgctcaccac ctctggctgt gccgcaggt cggcgggctg ccctgcgctg ccgggcagt 960
ggggacccag agccccgtgt gcgttgggtg tcacccaggg gccggtgct aggcaactca 1020
agccgtgccc gcgccttccc caatgggaag ctggagctgc tggtcaccga gccgggtgat 1080
ggtggcatct tcacctgat tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140
ctgactgtgg gtccccacc acctcctcag ctagccaaca gcaccagctg tgaccccccg 1200
cgggacgggg atcctgatgc tctcacccca cctcgcgtg cctctgcttc tgccaagggt 1260
gccgacactg ggcacctac cgacctggc gtccaggtga ctgagcacgg ggccacagct 1320
gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgta ccagatccag 1380
tacaacagct cggtgatga catcctcgtc tacaggatga tcccggcgga gagccgctcg 1440
ttcctgctga cggacctggc gtcaggccgg acctacgac tgtgcgtgct cgccgtgtat 1500
gaggacagcg ccacggggct cagggccacg cggcctgtgg gctgcgcccg cttctccacc 1560
gaacctgcgc tgcggccatg cggggcgccg cacgctccct tctgggcgg cagcatgatc 1620
atcgcgctgg gcggcgctcat cgtagcctcg gtactggtct tcatcttcgt gctgctaata 1680

cgctacaagg tgcacggcgg ccagccccc ggcaaggcca agattccgc gcctgttagc 1740
agcgtttgct ccagaccaa cggcgccctg ggcacacgc ccacgccgc cccgccgcc 1800
cggagccc cggcgctcag ggccacacc gtggtccagc tggactgcga gccctggggg 1860
ccggccacg aacctgtggg accctag 1887

<210> 4
<211> 365
<212> PRT
<213> Equus caballus

<400> 4
Thr Cys Cys Cys Ala Gly Ala Gly Gly Cys Cys Cys Ala Gly Gly Cys
1 5 10 15
Cys Gly Cys Gly Thr Cys Thr Gly Thr Cys Cys Thr Cys Cys Ala Cys
20 25 30
Gly Ala Gly Ala Thr Gly Cys Thr Cys Cys Ala Gly Cys Ala Gly Ala
35 40 45
Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr Thr Cys Cys Ala
50 55 60
Cys Ala Cys Ala Gly Ala Gly Cys Gly Cys Thr Cys Gly Thr Cys Thr
65 70 75 80
Gly Cys Thr Gly Cys Cys Thr Gly Gly Ala Ala Cys Ala Cys Gly Ala
85 90 95
Cys Cys Cys Thr Cys Cys Thr Gly Gly Ala Cys Gly Ala Ala Cys Thr
100 105 110
Cys Thr Gly Cys Ala Cys Gly Gly Gly Ala Cys Thr Cys Cys Thr Thr
115 120 125
Cys Gly Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys
130 135 140
Thr Gly Gly Ala Cys Ala Cys Cys Thr Gly Thr Thr Thr Gly Gly Ala
145 150 155 160
Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Gly Gly Ala Gly Ala Gly
165 170 175
Gly Ala Ala Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly
180 185 190

Gly Ala Ala Cys Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Ala Cys
 195 200 205

Ala Cys Thr Gly Gly Cys Cys Gly Thr Gly Ala Ala Gly Ala Gly Gly
 210 215 220

Thr Ala Cys Thr Thr Cys Cys Gly Gly Gly Gly Gly Ala Thr Cys Cys
 225 230 235 240

Ala Thr Cys Thr Cys Thr Ala Cys Cys Thr Gly Ala Ala Ala Gly Ala
 245 250 255

Gly Ala Ala Gly Ala Ala Ala Thr Ala Cys Ala Gly Thr Gly Ala Cys
 260 265 270

Thr Gly Thr Gly Cys Cys Thr Gly Gly Gly Ala Gly Ala Thr Thr Gly
 275 280 285

Thr Cys Cys Gly Ala Ala Thr Gly Gly Ala Ala Ala Thr Cys Ala Thr
 290 295 300

Gly Ala Gly Ala Thr Cys Cys Thr Thr Cys Thr Cys Thr Thr Cys Ala
 305 310 315 320

Thr Cys Ala Gly Cys Ala Ala Ala Cys Cys Thr Gly Cys Ala Ala Gly
 325 330 335

Gly Ala Ala Gly Gly Thr Thr Ala Ala Gly Ala Ala Thr Gly Ala Ala
 340 345 350

Gly Gly Ala Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly
 355 360 365

<210> 5

<211> 132

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
 1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
 20 25 30

Leu Ser Arg Asn Thr Leu Val Phe Pro Gln Glu Met Val Lys Gly Ser
 35 40 45

Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met Leu Gln
50 55 60

Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Thr Cys
65 70 75 80

Leu Leu Gln Val Val Gly Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser
85 90 95

Pro Ala Leu Thr Leu Arg Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu
100 105 110

Lys Glu Lys Lys Tyr Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp
115 120 125

Leu Gly Ser Ser
130

<210> 6

<211> 132

<212> PRT

<213> Equus caballus

<400> 6

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser
1 5 10 15

Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu
20 25 30

Arg Lys Gln Glu Thr Leu Arg Phe Pro Gln Glu Gln Leu Asp Gly Arg
35 40 45

Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu Gln Glu Met Leu Gln
50 55 60

Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Thr Cys
65 70 75 80

Leu Asp Glu Gln Thr Gly Glu Glu Glu Ser Ala Leu Gly Thr Val Gly
85 90 95

Pro Thr Leu Ala Val Lys Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu
100 105 110

Thr Glu Lys Lys Tyr Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp

115 120 125
 Leu Gly Ser Pro
 130

 <210> 7
 <211> 475
 <212> PRT
 <213> Homo sapiens

 <400> 7
 Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
 1 5 10 15
 Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
 20 25 30
 Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
 35 40 45
 Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys
 50 55 60
 Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys
 65 70 75 80
 Ala Gly Gly Thr Gly Ala Thr Thr Thr Cys Thr Gly Cys Cys Cys Thr
 85 90 95
 Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly
 100 105 110
 Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr
 115 120 125
 Thr Thr Thr Thr Ala Cys Ala Cys Ala Ala Gly Gly Gly Cys Thr Thr
 130 135 140
 Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr
 145 150 155 160
 Ala Gly Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala
 165 170 175
 Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr
 180 185 190

Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala
 195 200 205
 Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr
 210 215 220
 Thr Thr Gly Gly Thr Ala Thr Ala Gly Ala Gly Gly Ala Thr Gly Gly
 225 230 235 240
 Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys
 245 250 255
 Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Gly Cys Cys
 260 265 270
 Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala
 275 280 285
 Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Gly Ala
 290 295 300
 Gly Thr Ala Cys Ala Thr Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala
 305 310 315 320
 Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala Ala Thr Thr Cys Ala Gly
 325 330 335
 Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Gly Ala Gly
 340 345 350
 Gly Thr Thr Gly Thr Cys Gly Thr Ala Ala Thr Gly Gly Thr Ala Ala
 355 360 365
 Ala Gly Gly Gly Ala Thr Thr Thr Thr Thr Cys Thr Thr Ala Ala Gly
 370 375 380
 Cys Ala Cys Ala Ala Ala Ala Cys Thr Thr Cys Ala Ala Gly Ala Ala
 385 390 395 400
 Ala Ala Ala Gly Ala Gly Ala Ala Cys Ala Gly Ala Ala Gly Ala Ala
 405 410 415
 Ala Ala Gly Ala Gly Ala Ala Cys Thr Gly Cys Ala Ala Ala Ala Ala
 420 425 430
 Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly Thr Ala
 435 440 445

Ala Thr Cys Thr Ala Thr Thr Thr Ala Gly Cys Ala Gly Ala Ala Gly
 450 455 460

Ala Gly Thr Gly Ala Ala Ala Gly Cys Thr Gly
 465 470 475

<210> 8
 <211> 70
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_difference
 <222> (1)..(70)
 <223> n is the single letter notation for Asparagine

<400> 8
 shkaasvvhv tnkhctasss aawnttctgd rtracvvgat ndhdsrnyrs ykkyscawvr 60
 amrsyyssta 70

<210> 9
 <211> 112
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Interferon
 Delta-1 Precursor

<400> 9
 Leu Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln
 1 5 10 15
 Ser Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr
 20 25 30
 Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu His Gln Gln Leu Asp Asn
 35 40 45
 Leu Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu
 50 55 60
 Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile
 65 70 75 80
 His Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr

<400> 11

Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln
1 5 10 15

Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Trp Asn Met
20 25 30

Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln Leu Gln His
35 40 45

Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu Ser Ala Gly
50 55 60

Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe Gln Gly Ile
65 70 75 80

Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Val
85 90 95

Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln
100 105 110

<210> 12

<211> 65

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Interferon

<400> 12

Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser
1 5 10 15

Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln
20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys
35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu
50 55 60

Gln
65

<210> 13
<211> 110
<212> PRT
<213> Homo sapiens

<400> 13

Asn	Phe	Asp	Ile	Pro	Glu	Glu	Ile	Lys	Gln	Leu	Gln	Gln	Phe	Gln	Lys
1				5					10					15	

Glu	Asp	Ala	Ala	Leu	Thr	Ile	Tyr	Glu	Met	Leu	Gln	Asn	Ile	Phe	Ala
		20						25					30		

Ile	Phe	Arg	Gln	Asp	Ser	Ser	Ser	Thr	Gly	Trp	Asn	Glu	Thr	Ile	Val
		35					40					45			

Glu	Asn	Leu	Leu	Ala	Asn	Val	Tyr	His	Gln	Ile	Asn	His	Leu	Lys	Thr
	50					55					60				

Val	Leu	Glu	Glu	Lys	Leu	Glu	Lys	Glu	Asp	Phe	Thr	Arg	Gly	Lys	Leu
65					70					75					80

Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg	Ile	Leu	His	Tyr
				85						90				95	

Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr	Ile	Val		
		100						105					110		

<210> 14
<211> 109
<212> PRT
<213> Homo sapiens

<400> 14

Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Gly	Asn	Gln	Phe	Gln	Lys	Ala
1				5					10					15	

Glu	Thr	Ile	Pro	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Ile	Phe	Asn	Leu
			20					25					30		

Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu	Thr	Leu	Leu	Asp
		35					40					45			

Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp	Leu	Glu	Ala	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50 55 60
 Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn Glu Asp
 65 70 75 80
 Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu
 85 90 95
 Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 100 105

<210> 15
 <211> 110
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Interferon
 Alpha-1 Precursor

<400> 15
 Asp Phe Gly Phe Pro Gln Glu Lys Val Asp Ala Gln Gln Ile Lys Lys
 1 5 10 15
 Ala Gln Ala Ile Pro Val Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn
 20 25 30
 Ile Phe Thr Ser Lys Asp Ser Ser Ala Ala Trp Asn Ala Thr Leu Leu
 35 40 45
 Asp Ser Phe Cys Asn Asp Leu His Gln Gln Leu Asn Asp Leu Gln Gly
 50 55 60
 Cys Leu Met Gln Gln Val Gly Val Gln Glu Phe Pro Leu Thr Gln Glu
 65 70 75 80
 Asp Ala Leu Leu Ala Val Arg Lys Tyr Phe His Arg Ile Thr Val Tyr
 85 90 95
 Leu Arg Glu Lys Lys His Ser Pro Cys Ala Trp Glu Val Val
 100 105 110

<210> 16
 <211> 110
 <212> PRT
 <213> Rabbitt Interferon-omega20

<400> 16

Asp Phe Gln Phe Pro Arg Glu Val Val Asn Gly Ser Gln Phe Gln Lys
1 5 10 15

Asn Gln Thr Val Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Asn
20 25 30

Leu Leu His Thr Ala Arg Ser Ser Ala Ala Trp Asn Asn Thr Leu Leu
35 40 45

Glu Glu Leu His Thr Ala Leu His Gln Gln Leu Gln Gly Leu Glu Thr
50 55 60

Cys Leu Val Gln Ala Met Gly Glu Glu Asp Ser Val Leu Thr Ala Asp
65 70 75 80

Ser Pro Met Leu Met Leu Lys Arg Tyr Phe Gln Arg Ile Arg Leu Tyr
85 90 95

Leu Asp Glu Lys Lys His Ser Gly Cys Ala Trp Glu Leu Val
100 105 110

<210> 17

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus of
SEQ ID NO:1 and SEQ ID NOS:16-19

<400> 17

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val
35 40

<210> 18

<211> 184

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Interferon
Alpha-1 Precursor

<400> 18

Val	Ser	Leu	Leu	Met	Ala	Leu	Val	Val	Leu	Ser	Cys	His	Ser	Ile	Cys
1				5					10					15	

Ser	Leu	Gly	Cys	Asp	Leu	Pro	His	Thr	His	Ser	Leu	Gly	Asn	Thr	Arg
		20						25					30		

Val	Leu	Met	Leu	Leu	Gly	Gln	Met	Arg	Arg	Ile	Ser	Pro	Phe	Ser	Cys
		35					40						45		

Leu	Lys	Asp	Arg	Asn	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Val	Phe	Asp	Gly
	50					55					60				

Asn	Gln	Phe	Arg	Lys	Pro	Gln	Ala	Ile	Ser	Ala	Val	His	Glu	Thr	Ile
65					70					75					80

Gln	Gln	Ile	Phe	His	Leu	Phe	Ser	Thr	Asp	Gly	Ser	Ser	Ala	Ala	Trp
			85						90					95	

Asp	Glu	Ser	Leu	Leu	Asp	Lys	Leu	Tyr	Thr	Gly	Leu	Tyr	Gln	Gln	Leu
		100						105					110		

Thr	Glu	Leu	Glu	Ala	Cys	Leu	Ser	Gln	Glu	Val	Gly	Val	Glu	Glu	Thr
	115						120					125			

Pro	Leu	Met	Asn	Glu	Asp	Ser	Leu	Leu	Ala	Val	Arg	Arg	Tyr	Phe	Gln
	130					135					140				

Arg	Ile	Ala	Leu	Tyr	Leu	Gln	Glu	Lys	Lys	Tyr	Ser	Pro	Cys	Ala	Trp
145					150					155					160

Glu	Ile	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Ser	Ser	Thr	Asn
			165					170						175	

Leu	Pro	Ser	Glu	Gln	Ile	Asp	Asn
			180				

<210> 19

<211> 92

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus of
SEQ ID NO:4 and SEQ ID NOS:11, 13, 14, 21 and 22

<400> 19

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln
85 90

<210> 20

<211> 1752

<212> PRT

<213> Homo sapiens

<400> 20

Cys Gly Cys Cys Thr Gly Cys Cys Cys Cys Ala Ala Gly Thr Ala Cys
1 5 10 15

Thr Gly Thr Gly Thr Cys Thr Gly Cys Cys Ala Gly Ala Ala Thr Cys
20 25 30

Thr Gly Thr Cys Thr Gly Ala Gly Thr Cys Ala Cys Thr Gly Gly Gly
35 40 45

Gly Ala Cys Cys Cys Thr Gly Thr Gly Cys Cys Cys Cys Thr Cys Cys
50 55 60

Ala Ala Gly Gly Gly Gly Cys Thr Gly Cys Thr Cys Thr Thr Thr Gly
65 70 75 80

Thr Ala Cys Cys Cys Cys Cys Thr Gly Ala Thr Ala Thr Thr Gly Ala
85 90 95

Cys Cys Gly Gly Cys Gly Gly Ala Cys Ala Gly Thr Gly Gly Ala Gly
 100 105 110
 Cys Thr Gly Cys Gly Cys Cys Thr Gly Gly Gly Cys Gly Gly Cys Ala
 115 120 125
 Ala Cys Thr Thr Cys Ala Thr Cys Ala Thr Cys Cys Ala Cys Ala Thr
 130 135 140
 Cys Ala Gly Cys Cys Gly Cys Cys Ala Gly Gly Ala Cys Thr Thr Thr
 145 150 155 160
 Gly Cys Cys Ala Ala Cys Ala Thr Gly Ala Cys Gly Gly Gly Gly Cys
 165 170 175
 Thr Gly Gly Thr Gly Gly Ala Cys Cys Thr Gly Ala Cys Cys Cys Thr
 180 185 190
 Gly Thr Cys Cys Ala Gly Gly Ala Ala Cys Ala Cys Cys Ala Thr Cys
 195 200 205
 Ala Gly Cys Cys Ala Cys Ala Thr Cys Cys Ala Gly Cys Cys Cys Thr
 210 215 220
 Thr Thr Thr Cys Cys Thr Thr Thr Cys Thr Gly Gly Ala Cys Cys Thr
 225 230 235 240
 Cys Gly Ala Gly Ala Gly Cys Cys Thr Cys Cys Gly Cys Thr Cys Cys
 245 250 255
 Cys Thr Gly Cys Ala Thr Cys Thr Thr Gly Ala Cys Ala Gly Cys Ala
 260 265 270
 Ala Thr Cys Gly Gly Cys Thr Gly Cys Cys Ala Ala Gly Cys Cys Thr
 275 280 285
 Thr Gly Gly Gly Gly Ala Gly Gly Ala Cys Ala Cys Cys Cys Thr Cys
 290 295 300
 Cys Gly Gly Gly Gly Cys Cys Thr Gly Gly Thr Cys Ala Ala Cys Cys
 305 310 315 320
 Thr Gly Cys Ala Gly Cys Ala Cys Cys Thr Thr Ala Thr Cys Gly Thr
 325 330 335
 Gly Ala Ala Cys Ala Ala Cys Ala Ala Cys Cys Ala Gly Cys Thr Gly
 340 345 350

Gly Gly Cys Gly Gly Cys Ala Thr Cys Gly Cys Ala Gly Ala Thr Gly
 355 360 365
 Ala Gly Gly Cys Thr Thr Thr Thr Gly Ala Gly Gly Ala Cys Thr Thr
 370 375 380
 Cys Cys Thr Gly Cys Thr Gly Ala Cys Ala Thr Thr Gly Gly Ala Gly
 385 390 395 400
 Gly Ala Thr Cys Thr Gly Gly Ala Cys Cys Thr Cys Thr Cys Cys Thr
 405 410 415
 Ala Cys Ala Ala Cys Ala Ala Cys Cys Thr Cys Cys Ala Thr Gly Gly
 420 425 430
 Cys Cys Thr Gly Cys Cys Gly Thr Gly Gly Gly Ala Cys Thr Cys Cys
 435 440 445
 Gly Thr Gly Cys Gly Ala Cys Gly Cys Ala Thr Gly Gly Thr Cys Ala
 450 455 460
 Ala Cys Cys Thr Cys Cys Ala Cys Cys Ala Gly Cys Thr Gly Ala Gly
 465 470 475 480
 Cys Cys Thr Gly Gly Ala Cys Cys Ala Cys Ala Ala Cys Cys Thr Gly
 485 490 495
 Cys Thr Gly Gly Ala Thr Cys Ala Cys Ala Thr Cys Gly Cys Cys Gly
 500 505 510
 Ala Gly Gly Gly Cys Ala Cys Cys Thr Thr Thr Gly Cys Ala Gly Ala
 515 520 525
 Cys Cys Thr Gly Cys Ala Gly Ala Ala Ala Cys Thr Gly Gly Cys Cys
 530 535 540
 Cys Gly Cys Cys Thr Gly Gly Ala Thr Cys Thr Cys Ala Cys Cys Thr
 545 550 555 560
 Cys Cys Ala Ala Thr Cys Gly Gly Cys Thr Gly Cys Ala Gly Ala Ala
 565 570 575
 Gly Cys Thr Gly Cys Cys Cys Cys Cys Thr Gly Ala Thr Cys Cys Cys
 580 585 590
 Ala Thr Cys Thr Thr Thr Gly Cys Cys Cys Gly Cys Thr Cys Cys Cys
 595 600 605

Ala Gly Gly Cys Thr Thr Cys Gly Gly Cys Thr Thr Thr Gly Ala Cys
610 615 620

Ala Gly Cys Cys Ala Cys Ala Cys Cys Cys Thr Thr Thr Gly Cys Cys
625 630 635 640

Cys Cys Ala Cys Cys Cys Thr Thr Gly Thr Cys Cys Thr Thr Thr Ala
645 650 655

Gly Thr Thr Thr Thr Gly Gly Gly Gly Gly Thr Ala Ala Cys Cys Cys
660 665 670

Ala Cys Thr Thr Cys Ala Cys Thr Gly Cys Ala Ala Thr Thr Gly Thr
675 680 685

Gly Ala Gly Cys Thr Thr Cys Thr Cys Thr Gly Gly Cys Thr Gly Cys
690 695 700

Gly Gly Ala Gly Gly Cys Thr Cys Gly Ala Gly Cys Gly Gly Gly Ala
705 710 715 720

Cys Gly Ala Thr Gly Ala Cys Cys Thr Gly Gly Ala Ala Ala Cys Cys
725 730 735

Thr Gly Thr Gly Gly Cys Thr Cys Cys Cys Cys Ala Gly Gly Gly Gly
740 745 750

Gly Cys Cys Thr Cys Ala Ala Gly Gly Gly Thr Cys Gly Cys Thr Ala
755 760 765

Cys Thr Thr Cys Thr Gly Gly Cys Ala Thr Gly Thr Gly Cys Gly Thr
770 775 780

Gly Ala Gly Gly Ala Gly Gly Ala Gly Thr Thr Thr Gly Thr Gly Thr
785 790 795 800

Gly Cys Gly Ala Gly Cys Cys Gly Cys Cys Thr Cys Thr Cys Ala Thr
805 810 815

Cys Ala Cys Cys Cys Ala Gly Cys Ala Cys Ala Cys Ala Cys Ala Cys
820 825 830

Ala Ala Gly Thr Thr Gly Cys Thr Gly Gly Thr Thr Cys Thr Gly Gly
835 840 845

Ala Gly Gly Gly Cys Cys Ala Gly Gly Cys Gly Gly Cys Cys Ala Cys
850 855 860

Ala Cys Thr Cys Ala Ala Gly Thr Gly Cys Ala Ala Ala Gly Cys Cys
 865 870 875 880
 Ala Thr Thr Gly Gly Gly Gly Ala Cys Cys Cys Cys Ala Gly Cys Cys
 885 890 895
 Cys Cys Cys Thr Thr Ala Thr Cys Cys Ala Cys Thr Gly Gly Gly Thr
 900 905 910
 Ala Gly Cys Cys Cys Cys Cys Gly Ala Thr Gly Ala Cys Cys Gly Cys
 915 920 925
 Cys Thr Gly Gly Thr Ala Gly Gly Gly Ala Ala Cys Thr Cys Cys Thr
 930 935 940
 Cys Ala Ala Gly Gly Ala Cys Cys Gly Cys Thr Gly Thr Cys Thr Ala
 945 950 955 960
 Thr Gly Ala Cys Ala Ala Thr Gly Gly Cys Ala Cys Cys Cys Thr Gly
 965 970 975
 Gly Ala Cys Ala Thr Cys Thr Thr Cys Ala Thr Cys Ala Cys Cys Ala
 980 985 990
 Cys Ala Thr Cys Thr Cys Ala Gly Gly Ala Cys Ala Gly Thr Gly Gly
 995 1000 1005
 Thr Gly Cys Cys Thr Thr Cys Ala Cys Cys Thr Gly Cys Ala Thr Thr
 1010 1015 1020
 Gly Cys Thr Gly Cys Cys Ala Ala Thr Gly Cys Thr Gly Cys Cys Gly
 1025 1030 1035 1040
 Gly Ala Gly Ala Gly Gly Cys Cys Ala Cys Gly Gly Cys Cys Ala Thr
 1045 1050 1055
 Gly Gly Thr Gly Gly Ala Gly Gly Thr Cys Thr Cys Cys Ala Thr Cys
 1060 1065 1070
 Gly Thr Cys Cys Ala Gly Cys Thr Gly Cys Cys Ala Cys Ala Cys Cys
 1075 1080 1085
 Thr Cys Ala Gly Cys Ala Ala Cys Ala Gly Cys Ala Cys Cys Ala Gly
 1090 1095 1100
 Cys Cys Gly Cys Ala Cys Thr Gly Cys Ala Cys Cys Cys Cys Cys Cys
 1105 1110 1115 1120

Ala Ala Gly Thr Cys Cys Cys Gly Cys Cys Thr Cys Thr Cys Ala Gly
 1125 1130 1135

Ala Cys Ala Thr Cys Ala Cys Thr Gly Gly Cys Thr Cys Cys Ala Gly
 1140 1145 1150

Cys Ala Ala Gly Ala Cys Cys Ala Gly Cys Cys Gly Gly Gly Gly Ala
 1155 1160 1165

Gly Gly Thr Gly Gly Ala Gly Gly Cys Ala Gly Thr Gly Gly Gly Gly
 1170 1175 1180

Gly Cys Gly Gly Ala Gly Ala Gly Cys Cys Thr Cys Cys Cys Ala Ala
 1185 1190 1195 1200

Ala Ala Gly Cys Cys Cys Cys Cys Cys Gly Gly Ala Ala Cys Gly Gly
 1205 1210 1215

Gly Cys Thr Gly Thr Gly Cys Thr Thr Gly Thr Gly Thr Cys Thr Gly
 1220 1225 1230

Ala Ala Gly Thr Gly Ala Cys Cys Ala Cys Cys Ala Cys Cys Thr Cys
 1235 1240 1245

Gly Gly Cys Cys Cys Thr Gly Gly Thr Cys Ala Ala Gly Thr Gly Gly
 1250 1255 1260

Thr Cys Thr Gly Thr Cys Ala Gly Cys Ala Ala Gly Thr Cys Ala Gly
 1265 1270 1275 1280

Cys Ala Cys Cys Cys Cys Gly Gly Gly Thr Gly Ala Ala Gly Ala Thr
 1285 1290 1295

Gly Thr Ala Cys Cys Ala Gly Cys Thr Gly Cys Ala Gly Thr Ala Cys
 1300 1305 1310

Ala Ala Cys Thr Gly Cys Thr Cys Thr Gly Ala Cys Gly Ala Thr Gly
 1315 1320 1325

Ala Gly Gly Thr Ala Cys Thr Gly Ala Thr Thr Thr Ala Cys Ala Gly
 1330 1335 1340

Gly Ala Thr Gly Ala Thr Cys Cys Cys Ala Gly Cys Cys Thr Cys Cys
 1345 1350 1355 1360

Ala Ala Cys Ala Ala Gly Gly Cys Cys Thr Thr Cys Gly Thr Gly Gly
 1365 1370 1375

Thr Cys Ala Ala Cys Ala Ala Cys Cys Thr Gly Gly Thr Gly Thr Cys
 1380 1385 1390
 Ala Gly Gly Gly Ala Cys Thr Gly Gly Cys Thr Ala Cys Gly Ala Cys
 1395 1400 1405
 Thr Thr Gly Thr Gly Thr Gly Thr Gly Cys Thr Gly Gly Cys Cys Ala
 1410 1415 1420
 Thr Gly Thr Gly Gly Gly Ala Thr Gly Ala Cys Ala Cys Ala Gly Cys
 1425 1430 1435 1440
 Cys Ala Cys Gly Ala Cys Ala Cys Thr Cys Ala Cys Gly Gly Cys Cys
 1445 1450 1455
 Ala Cys Cys Ala Ala Cys Ala Thr Cys Gly Thr Gly Gly Gly Cys Thr
 1460 1465 1470
 Gly Cys Gly Cys Cys Cys Ala Gly Thr Thr Cys Thr Thr Cys Ala Cys
 1475 1480 1485
 Cys Ala Ala Gly Gly Cys Thr Gly Ala Cys Thr Ala Cys Cys Cys Gly
 1490 1495 1500
 Cys Ala Gly Thr Gly Cys Cys Ala Gly Thr Cys Cys Ala Thr Gly Cys
 1505 1510 1515 1520
 Ala Cys Ala Gly Cys Cys Ala Gly Ala Thr Cys Thr Gly Gly Gly
 1525 1530 1535
 Cys Gly Gly Cys Ala Cys Cys Ala Thr Gly Ala Thr Cys Cys Thr Gly
 1540 1545 1550
 Gly Thr Cys Ala Thr Cys Gly Gly Gly Gly Cys Ala Thr Cys Ala
 1555 1560 1565
 Thr Cys Gly Thr Gly Gly Cys Cys Ala Cys Gly Cys Thr Gly Cys Thr
 1570 1575 1580
 Gly Gly Thr Cys Thr Thr Cys Ala Thr Cys Gly Thr Cys Ala Thr Cys
 1585 1590 1595 1600
 Cys Thr Cys Ala Thr Gly Gly Thr Gly Cys Gly Cys Thr Ala Cys Ala
 1605 1610 1615
 Ala Gly Gly Thr Cys Thr Gly Cys Ala Ala Cys Cys Ala Cys Gly Ala
 1620 1625 1630

Gly Gly Cys Cys Cys Cys Cys Ala Gly Cys Ala Ala Gly Ala Thr Gly
 1635 1640 1645

Gly Cys Ala Gly Cys Gly Gly Cys Cys Gly Thr Gly Ala Gly Cys Ala
 1650 1655 1660

Ala Thr Gly Thr Gly Thr Ala Cys Thr Cys Gly Cys Ala Gly Ala Cys
 1665 1670 1675 1680

Cys Ala Ala Cys Gly Gly Cys Gly Cys Cys Cys Ala Gly Cys Cys Ala
 1685 1690 1695

Cys Cys Gly Cys Cys Thr Cys Cys Ala Ala Gly Cys Ala Gly Cys Gly
 1700 1705 1710

Cys Ala Cys Cys Ala Gly Cys Cys Gly Gly Gly Gly Cys Cys Cys Cys
 1715 1720 1725

Gly Cys Cys Gly Cys Ala Gly Gly Gly Cys Cys Cys Gly Cys Cys Gly
 1730 1735 1740

Ala Ala Gly Gly Thr Gly Gly Thr
 1745 1750

<210> 21

<211> 581

<212> PRT

<213> Homo sapiens

<400> 21

Ala Val Val Asp Ala Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser
 1 5 10 15

Glu Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro
 20 25 30

Pro Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe
 35 40 45

Ile Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val
 50 55 60

Asp Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser
 65 70 75 80

Phe Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg
 85 90 95

Leu Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln
 100 105 110
 His Leu Ile Val Asn Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala
 115 120 125
 Phe Glu Asp Phe Leu Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn
 130 135 140
 Asn Leu His Gly Leu Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu
 145 150 155 160
 His Gln Leu Ser Leu Asp His Asn Leu Leu Asp His Ile Ala Glu Gly
 165 170 175
 Thr Phe Ala Asp Leu Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn
 180 185 190
 Arg Leu Gln Lys Leu Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala
 195 200 205
 Ser Ala Leu Thr Ala Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe
 210 215 220
 Gly Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg
 225 230 235 240
 Leu Glu Arg Asp Asp Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu
 245 250 255
 Lys Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu
 260 265 270
 Pro Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly
 275 280 285
 Gln Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu
 290 295 300
 Ile His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg
 305 310 315 320
 Thr Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser
 325 330 335
 Gln Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu
 340 345 350

Ala Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser
 355 360 365
 Asn Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile
 370 375 380
 Thr Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly
 385 390 395 400
 Glu Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val
 405 410 415
 Thr Thr Thr Ser Ala Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro
 420 425 430
 Arg Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val
 435 440 445
 Leu Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn
 450 455 460
 Asn Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp
 465 470 475 480
 Asp Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala
 485 490 495
 Gln Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser
 500 505 510
 Gln Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val
 515 520 525
 Ala Thr Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val
 530 535 540
 Cys Asn His Glu Ala Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val
 545 550 555 560
 Tyr Ser Gln Thr Asn Gly Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro
 565 570 575
 Ala Gly Ala Pro Pro
 580

<210> 22

<211> 788
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown Organism: KIAA_predicted

<400> 22

Met Glu Thr Leu Leu Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala
1 5 10 15

Val Val Asp Ala Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu
20 25 30

Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro
35 40 45

Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile
50 55 60

Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp
65 70 75 80

Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe
85 90 95

Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu
100 105 110

Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His
115 120 125

Leu Ile Val Asn Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe
130 135 140

Glu Asp Phe Leu Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn
145 150 155 160

Leu His Gly Leu Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His
165 170 175

Gln Leu Ser Leu Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr
180 185 190

Phe Ala Asp Leu Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg
195 200 205

Leu Gln Lys Leu Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser

210		215		220	
Ala Leu Thr Ala Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly					
225		230		235	240
Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu					
	245		250		255
Glu Arg Asp Asp Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys					
	260		265		270
Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro					
	275		280		285
Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln					
	290		295		300
Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile					
305		310		315	320
His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr					
	325		330		335
Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln					
	340		345		350
Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala					
	355		360		365
Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn					
	370		375		380
Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr					
385		390		395	400
Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu					
	405		410		415
Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr					
	420		425		430
Thr Thr Ser Ala Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg					
	435		440		445
Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu					
	450		455		460
Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn					

465		470		475		480
Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp						
	485		490		495	
Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln						
	500		505		510	
Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln						
	515		520		525	
Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala						
	530		535		540	
Thr Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys						
545		550		555		560
Asn His Glu Ala Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr						
	565		570		575	
Ser Gln Thr Asn Gly Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala						
	580		585		590	
Gly Ala Pro Pro Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu						
	595		600		605	
Leu Asp Phe Thr Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser						
	610		615		620	
Ser Ser Leu Gly Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp						
625		630		635		640
Arg Ile Pro Pro Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu						
	645		650		655	
Met Gly Ala Phe Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu						
	660		665		670	
Leu Leu Asp Ser Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala						
	675		680		685	
Arg Gly His His Ser Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala						
	690		695		700	
Arg Ala Arg Ser Leu Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg						
705		710		715		720
Ser His Ser Phe Asp Met Gly Asp Phe Ala Ala Ala Ala Gly Gly Val						

725

730

735

Val Pro Gly Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr
740 745 750

Lys Arg Ser Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser
755 760 765

Asp Leu Val Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met
770 775 780

Glu Ser Thr Val
785